

Fig. 1

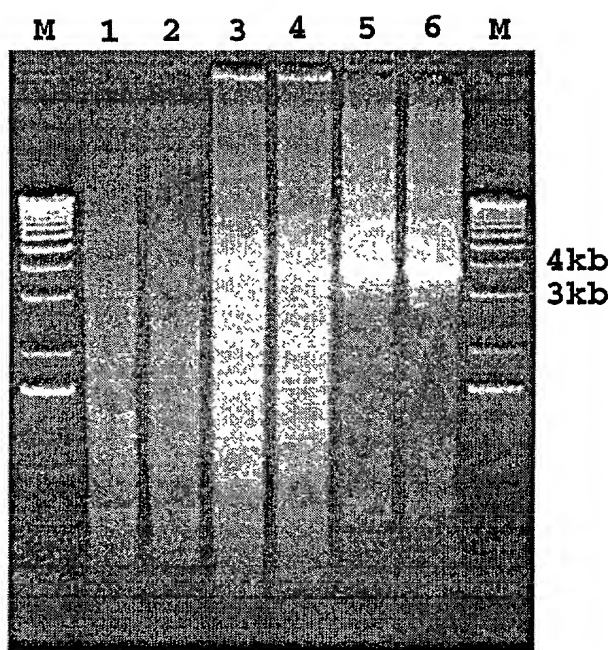


Fig. 2A

Burma	GGEIGHQRPVPIPRGNPDANDTDLAAPPSCQISAFHQLAEELGHRPVPVAAVLPPCPELEQGLLYLPQELTCTDSDSVVTFELTDIVHCRMAAPSQKAVL	100
D11092 ChinaA.....	100
D11093 ChinaC.....	100
HEV-T1 ChinaR.TI.N.....D.....F.Y.....A.I.....M.....S.L.....R.....	100
Hetian ChinaA.....	100
Hyderabad IndiaA.....	100
KS2-87 ChinaA.....	100
L25547 ChinaA.....	100
Madras IndiaA.....	100
MexicoV.....G.....GV.....R.....I.....AS.....R.S.....V.....	100
MyanmarR.V.....A.....	100
NepalA.....	100
SAR-55 PakistanA.....	100
Swine HEV USAV.H.....Q.LG.Q.....Y.....A.....M.....VS.LV.....	100
US1 USAV.XH.....Q.LG.Q.....Y.....A.....M.....VS.LV.....	100
US2 USAV.H.....Q.LG.Q.....Y.....A.....M.....VS.LV.....	100
X98292 IndiaT.....	100
Avian HEV USA	LVRPDAAA.AGVL.A-.DT.G.LDI.AHTDV.AVLT.AI.A.LEL.IN.G.V.....M.AR.DGR.E.KLQ.S.T.....L..TS.L.I.99	99
Burma	STLVGRYGGRTKLYNASHDVRDSLARFIPAIGPVQVTTCELYELVEAMVERKGQDGSVLELDLNCNRDVSRIFFQKDCNKFTTGETIAHGKVGQGISAW	200
D11092 ChinaR.....	200
D11093 ChinaPAG.....	200
HEV-T1 ChinaR.....E.A.T.....G.NH.....EL.IN.....S.....	200
Hetian ChinaH.R.....	200
Hyderabad IndiaR.....	200
KS2-87 ChinaR.....	200
L25547 ChinaR.....	200
Madras India	T.....R.....T.....S.E.....I.....EHM.....A.....V.....	200
MexicoR.R.D.G.T.A.....TL.R.TA.....F.....S.....	200
MyanmarR.....	200
NepalR.....C.....	200
SAR-55 PakistanR.....	200
Swine HEV USAR.....E.A.....E.....T.....A.....	200
US1 USAR.....E.A.....E.....T.....A.....	200
US2 USAR.....E.A.....E.....T.....RA.....	200
X98292 IndiaR.....	200
Avian HEV USA	N.....KA.....-PEVEY.LM.TI.Q.WHH.....INFS.L.YA.NC.....LS.....LIVH.....QDA.C.....A.....LDDPV.....198	198
Burma	SKTFCALFGPWFRATEKAILALLPQGVFYGDADFDDTVF-SAAVAAAKASMVFNDFSEFSDTONNFSGLGLECAIMEECGMPQWLIRLYHLIRSANILQAP	299
D11092 China	299
D11093 China	299
HEV-T1 ChinaE.A.APN.....YE.....L-A.....G.PGCK.....	299
Hetian ChinaR.....	299
Hyderabad India	299
KS2-87 China	299
L25547 China	299
Madras IndiaP.....	299
MexicoS.A.....Y.S.....G.SHA.....	299
Myanmar	299
Nepal	299
SAR-55 Pakistan	299
Swine HEV USAE.....PNI.....YEES.-A..SG.GSC.....	299
US1 USAE.....PNI.....YEES.-A..SG.GSC.....	299
US2 USAE.....PNI.....YEES.-A..SG.GSC.....	299
X98292 India	299
Avian HEV USA	P.L.....HLV.G.P.PY.....LYTEADLHRSVLC.PAGHL.....V.D.....EL.RRF.....D.WVA.....V.Y.L.V.....298	298

Burma	KESLRGFWKKHSGEPGTL	WMNTVWNMAVITHCYDFRDFQVAAAFKDDSI	VLCSYRSPGA	AVLIAGCGLKLVDFRIGLYAGVVVAPGLGALPDVVR	399
D11092 China	L.....	399
D11093 China	L.....	399
HEV-T1 China	A..E..LK.....	V...D...RD.....T.....	399
Hetian China	L.....	399
Hyderabad India	L.....MR.....	399
KS2-87 China	L.....	399
L2547 China	L.....	399
Madras India	L.....	399
Mexico	S.....	I.A..E..L.....	V.....GS.....A.....	399
Myanmar	399
Nepal	399
SAR-55 Pakistan	399
Swine HEV USA	K.....	I.A..E..R.....	V...D...RN..A.....Y.....T.....	399
US1 USA	K.....	I.A..E..R.....	V...D...RN..A.....Y.....T.....	399
US2 USA	K.....	I.A..E..R.....	V...D...RN..A.....Y.....T.....	399
X98292 India	399
Avian HEV USA	A...C.....	T.LH.V.E.DRPS.LC.....	V.V.E.SV.AR.EGVS.V.D...M.DKTG.C.AFSNLLIF...A.VVC.LL.Q	398
Burma	AGRLTEKNWGPGERAEQLRAVSDFLRKL	TNVQAQ--MCV	DDVVS	RVYGVSPGLVHNLIGMLQAVADGKAHFTESVKPVLDLTNSILCRVE	487
D11092 China	487
D11093 China	487
HEV-T1 China	S.....	K.....C.....	--V...Q.....TI.....TI.....S.IY...	487
Hetian China	487
Hyderabad India	487
KS2-87 China	487
L2547 ChinaS.....	487
Madras India	487
Mexico	S.....	D.....	Q...R...-I..E...TIG...I...H.MH.S.	487
Myanmar	487
Nepal	487
SAR-55 Pakistan	487
Swine HEV USA	S.....	C..G.....-V.....TI.....TI.....IQ...	487
US1 USA	S.....	C..G.....-V.....TI.....TI.....IQ...	487
US2 USA	S.....	C..G.....-V.....TI.....NI.....IQ...	487
X98292 India	487
Avian HEV USA	W....D....	DIQ.MOD.EQ.CK..	VARVVTQKGKMLTIQL.AGY...EV.M.EVVW.A.K.C.AARETLVTNPL...N.SKE----	D.	484

Fig. 3A

[illegible]

Fig. 3C

Burma	CCCTATATTTCATCCAACCAACCCCTTTCGCCCGGATGTACCGCTCGGGCGGGCTGGACCTGTTTCGCCAACCCGCCGACCACTCCGGCTCGCTTGGCGTGACC	546
Hyderabad IndiaGA.....T.....C.....	546
Madras IndiaT.....T.....C.....	546
X98292 IndiaC.....C.....	546
HETIAN ChinaT.....T.....A.....TC	546
SAR.55 PakistanT.....A.C.TG.....T.....CC.....A.....G.....T.....	546
MexicoT.....T.....T.....T.....T.....T.....	546
KS2.87 ChinaT.....T.....T.....T.....T.....T.....	546
D11093 ChinaT.....T.....T.....T.....T.....T.....	546
D11092 ChinaT.....T.....T.....T.....T.....T.....	546
MyanmarT.....T.....T.....T.....T.....T.....	546
HEV-T1 ChinaAT.T.CA.TC.A.C.....A.....G.....CCC.....G.G.AAT.....T.....	541
US2 USAG.....GTTT.ACAAC.....A.....CCC.....A.G.G.....C.C.T.N.....	543
US1 USAG.....GTTT.ACAAC.....A.....CCC.....A.G.G.....C.C.....T.....	543
NepalTG.....GTTT.ACAAC.....GT.....CC.....A.G.G.....C.C.T.....	546
Swine HEV USATG.....GTTT.ACAAC.....GT.....CC.....A.G.G.....C.C.T.....	543
Avian HEV USA	-----G.....A.GCA.GCG.G.CCAG.....G.....GT.....A.T.CA..C.A.....A.CACT. 445	

***ORF3 (HEV)

Burma	AGGCCAGCGCCCGCTTGCCTCAGTGTGCTAGACCTACACAGCTGGGGCGCGCTACCGCGGTGCTCCGGCCCATGACACCCCGCAGTGCCTGATGTGCG	625
Hyderabad IndiaC.....C.....C.....T.....	625
Madras IndiaA.....C.....C.....T.....	625
X98292 IndiaT.....T.....T.....T.....T.....T.....	625
HETIAN ChinaT.....T.....T.....T.....T.....T.....	625
SAR.55 PakistanT.....T.....T.....T.....T.....T.....	625
MexicoT.....T.....T.....T.....T.....T.....	625
KS2.87 ChinaT.....T.....T.....T.....T.....T.....	625
D11093 ChinaT.....T.....T.....T.....T.....T.....	625
D11092 ChinaT.....T.....T.....T.....T.....T.....	625
MyanmarT.....T.....T.....T.....T.....T.....	625
HEV-T1 ChinaT.....T.....T.....T.....T.....T.....	625
US2 USAT.....T.....T.....T.....T.....T.....	625
US1 USAT.....T.....T.....T.....T.....T.....	625
NepalT.....T.....T.....T.....T.....T.....	625
Swine HEV USAT.....T.....T.....T.....T.....T.....	625
Avian HEV USAA.....AG.GA.....TC.CC.....C.T.C.A.AC.T.TCA.C.CGCA.GT..T.GCA.G.A.A.....A. 500	

***ORF3
(avian HEV)

RdelaHEV Primer

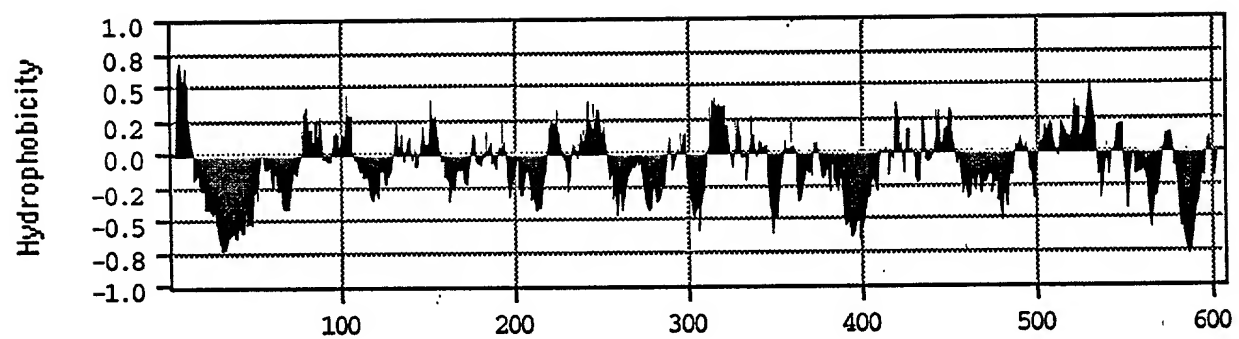


Fig. 4

Fig. 5B

Burma	ASLVTIPSERLHYRNOCHRSVETSQVAEEAT	SOLVHLCINGSLNSYNTPTTCALCLLDPA	LELEFPMLTFCNTNTRVSRYSSTARHLR	RGADCTAELTTTAATRFMKDLYFTSTNO	360
Hyderabad IndiaP.....	360
Madras IndiaP.....	360
HETIAN ChinaH.....	360
SAR.55 PakistanP.....	360
MexicoP.....	359
KS5.87 ChinaP.....	360
D11093 ChinaP.....	360
D11092 ChinaP.....	360
HEV.T1 ChinaP.....	358
MyanmarT.....	360
US2 USAP.....	360
US1 USAP.....	360
NepalP.....	360
Swine HEV USAT.....	360
U22532 IndiaP.....	360
AKL.90 IndiaP.....	360
MoroccoP.....	360
Egypt93P.....	360
Egypt94P.....	360
Avian HEV USAP.....	360
Burma	GL.T.H.A.K.N.....	VS.FQ.D.....	ML.V.V.TFW.....	SV...P.MV...IK.QL..S.....	A.T.VKV..P.TIKADPS-.TI..A.A..A.VRWGIG.A
Hyderabad IndiaVGEIGRGIALTFNLADTL	LGCLPTELISSAGQOLFYSRPVVSANGEPT	VKLITSVENAQDQKIAIPHDIDLGESRV	VIQDYNQHEQDRPTTSPAPSRPFSVL	RANDVLMLS---LT
Madras IndiaR.....	476
HETIAN ChinaN.....	476
SAR.55 PakistanL.....	476
MexicoV.....	475
KS5.87 ChinaD.....	476
D11093 China	476
D11092 China	476
HEV.T1 ChinaV.....	474
MyanmarH.....	476
US2 USAT.....	476
US1 USAT.....	476
NepalV.....	476
Swine HEV USAT.....	476
U22532 IndiaD.....	476
AKL.90 India	476
Morocco	476
Egypt93	476
Egypt94	476
Avian HEV USA	ED...H.LGV.....	V.....	ST.LRA.S.Y.....	GN.....E.....N..D.VN..P.MV.....	T.T.TC..G...VD...S.A..K.ALGT..SG...RITGSMQY

Burma	AAEYDQSTYGSSTGCPVTVSDSVTLVNVATCAQAVARSLDWTNVLDRPISTIQOYS--KTFFVLPLRCLSEWAGTTKAGVPYVNTTASDQLLVENACHRVAISTYTTSLGAPV3	594
Hyderabad India--I.....RP.....	594
Madras India	594
HETIAN ChinaT.....	594
SAR.55 Pakistan	594
MexicoI.....P.VE.....	593
KS5.87 China	594
D11093 chinaC.....	594
D11092 China	594
HEV.T1 ChinaT.....G.S.....S.....Y.....	592
MyanmarT.....N.M.....T.....P.....	594
US2 USAT.....N.M.....T.....S.....Y.....	594
US1 USAT.....N.M.....T.....S.....K.Y.....	594
NepalT.....N.M.....T.....S.....	594
Swine HEV USAT.....N.M.....T.....S.....Y.....	594
U22532 India	594
AKL.90 India	594
Morocco	594
Egypt93	594
Avian HEV USAVTNAELLPOSV.Q.YFGAGSTMVH.LI..VR.P.S.V...A.V.VQVK.VDAS.GSNR.AA..AF...AV.GP--QG...F.Q..B.HQEWIYFLQM--ES.VWYA..NML-QK---	538
Burma	ISAVAVLAPHSALELLEDITLDYPARANTDDPCPCRPLOCCAFQS---TVAELOQLKMKVKTREL--	660
Hyderabad IndiaG.....	655
Madras India	660
HETIAN ChinaM.....	660
SAR.55 PakistanV.....M.....	660
MexicoA.....S.....F..G.....A.....	659
KS5.87 ChinaT.....M.....	660
D11093 chinaM.....	660
D11092 ChinaM.....	660
HEV.T1 ChinaV..GV.....A.....A.....G.....Y.....	658
MyanmarC.....	660
US2 USAG.....V.....I.....T.....	660
US1 USAG.....V.....V.....I.....T.....S.....	660
NepalG.....V.....V.....I.....S.....	660
Swine HEV USAG.....	660
U22532 IndiaF.....	660
AKL.90 India	660
Morocco	660
Egypt93	660
Avian HEV USA-SDTSI.FEVRPIQASDQ--PWFLAH..GG.D.TT.L....RT.CR.APEDQSP.TR..LDRLSR.FPSPP	606

Avian HEV USA	ACATGTCGTGGTTTTTGGGGTTTTAGGTTGATTTCTGTATCTGGGCGTAATGCCCCCTATGTTTAATTTA70	
Burma	-----T....G.....T.....CT.C...C-..G29	
D11092 China	-----T....G.....T.....CT.C...C-..G29	
D11093 China	-----T....G.....T.....CT.C...C-..G29	
HEV-T1 China	-----T....G.....T.....CT.C.GCC..G30	
Hetian China	-----T....G.....T.....CT.C...C-..G29	
Hyderabad India	-----T....G.....T.....CT.C.C.C-..G29	
L25547 China	-----T....G.....T.....CT.T...C-..G29	
Mexico	-----T....GGC-----T.....A.CTAC..AT..C.G32	
Myanmar	-----T..C.G.....T.....CT.C...C-..G29	
Nepal	-----T....G.....T.....CT.C.C.C-..G29	
SAR-55 Pakistan	-----T....G.....T.....CT.C...C-..G29	
Swine HEV USA	-----A...C-----TT.T-----G...CC.TCA..GC..C31	
US1 USA	-----A...C-----TT.T-----G...CC.TCGC.G..CT31	
US2 USA	-----A...C-----CT.T-----G...CC.TCG..G...C31	
X98292 India	-----T....G.....T.....CT.C...C-..G29	
Avian HEV USA	TTGTGATTTTATAACTGTTTCATTGATTATTTATGAAATCCTCCCATCTCGGGCATAGT	130
Burma	...-----C-----T....C-.C...C..CGT...G.G.TC.CT.	65
D11092 China	...-----C-----T....C-.CT...C..CGT...G.G.TC.CT.	65
D11093 China	...-----C-----T....C-.CT...C..CGT...G.G.TC.CT.	65
HEV-T1 China	..T-----C-----T....C-CCT...C..CGTC...G.G.TC.CT.	68
Hetian China	...-----C-----T....C-.C...C..CGT...G.G.TC.CT.	65
Hyderabad India	...-----C-----T....C-.C...C..CGT...G.G.TC.CT.	65
L25547 China	...-----C-----T....C-.CT...C..CGT.T.G.G.TC.CT.	65
Mexico	C.---...CC-----T....C-C.T...C.CGGTC...G.G.TC.CT.	74
Myanmar	...-----C-----T....C-....C..CGT...G.G.TC.CT.	65
Nepal	...-----C-----T....C-.CT...C..CGT...G.G.TC.CT.	65
SAR-55 Pakistan	...-----C-----T....	39
Swine HEV USA	C.---...GG-----T....C-....C..CTT...G.G.TC.CT..	72
US1 USA	C.---...GGC-----T....C-.C...C..CTT...G.G.TC.CT..	72
US2 USA	...-----CGC-----T....C-....C..CTT...G.G.TC.CT..	72
X98292 India	C.---...C-----T....C-.CT...C..CGT.T.G.G.TC.CT.	65

Fig. 6

Fig. 7

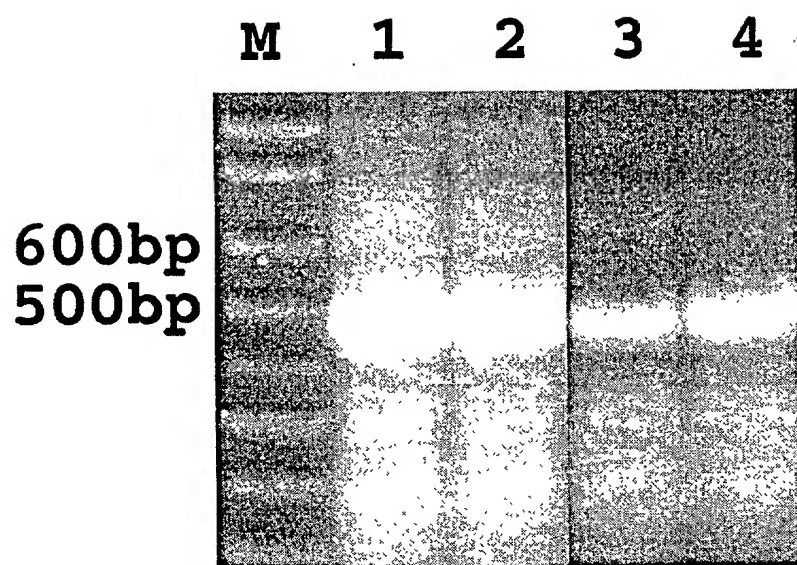


Fig. 8A

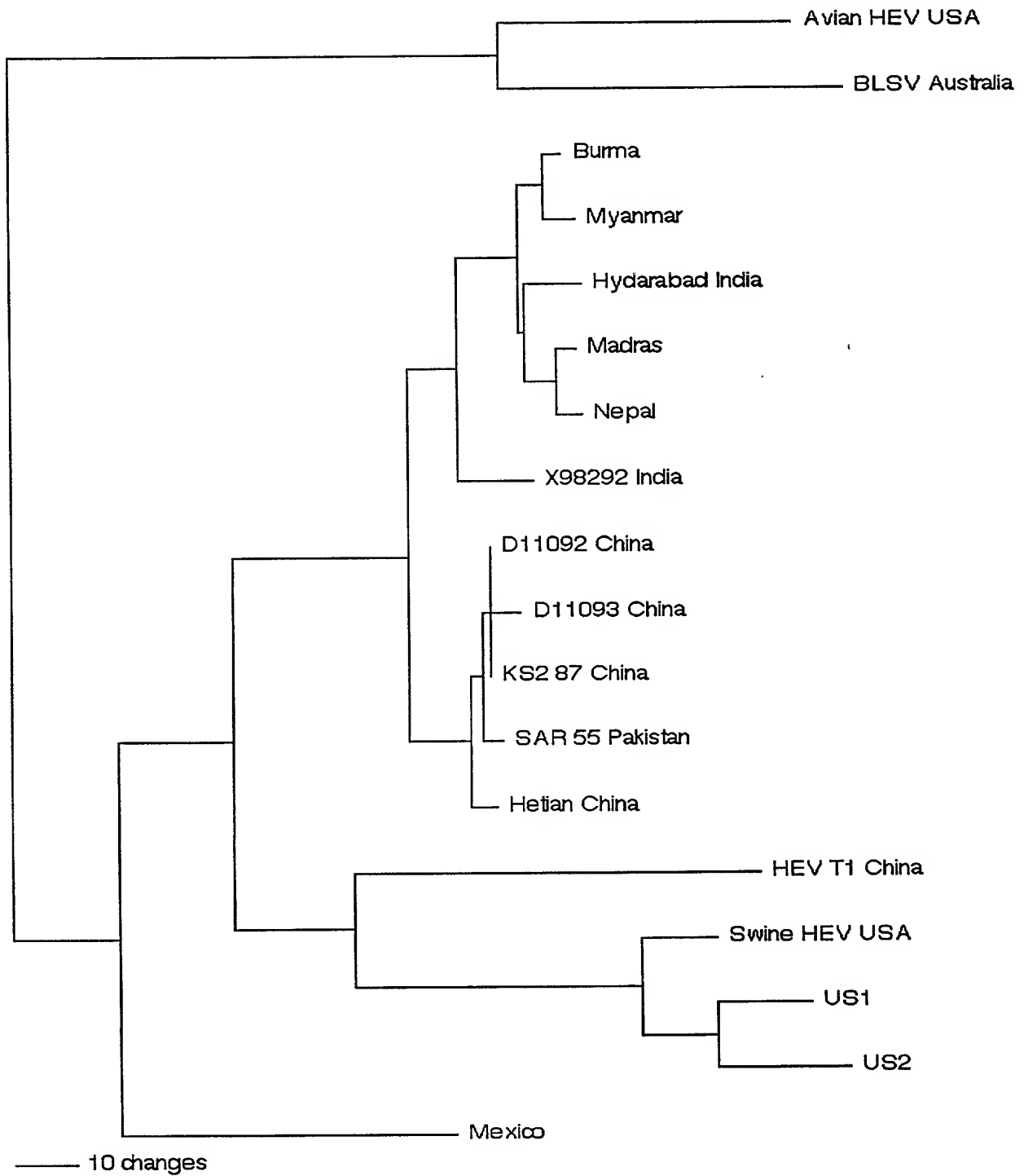


Fig. 8B

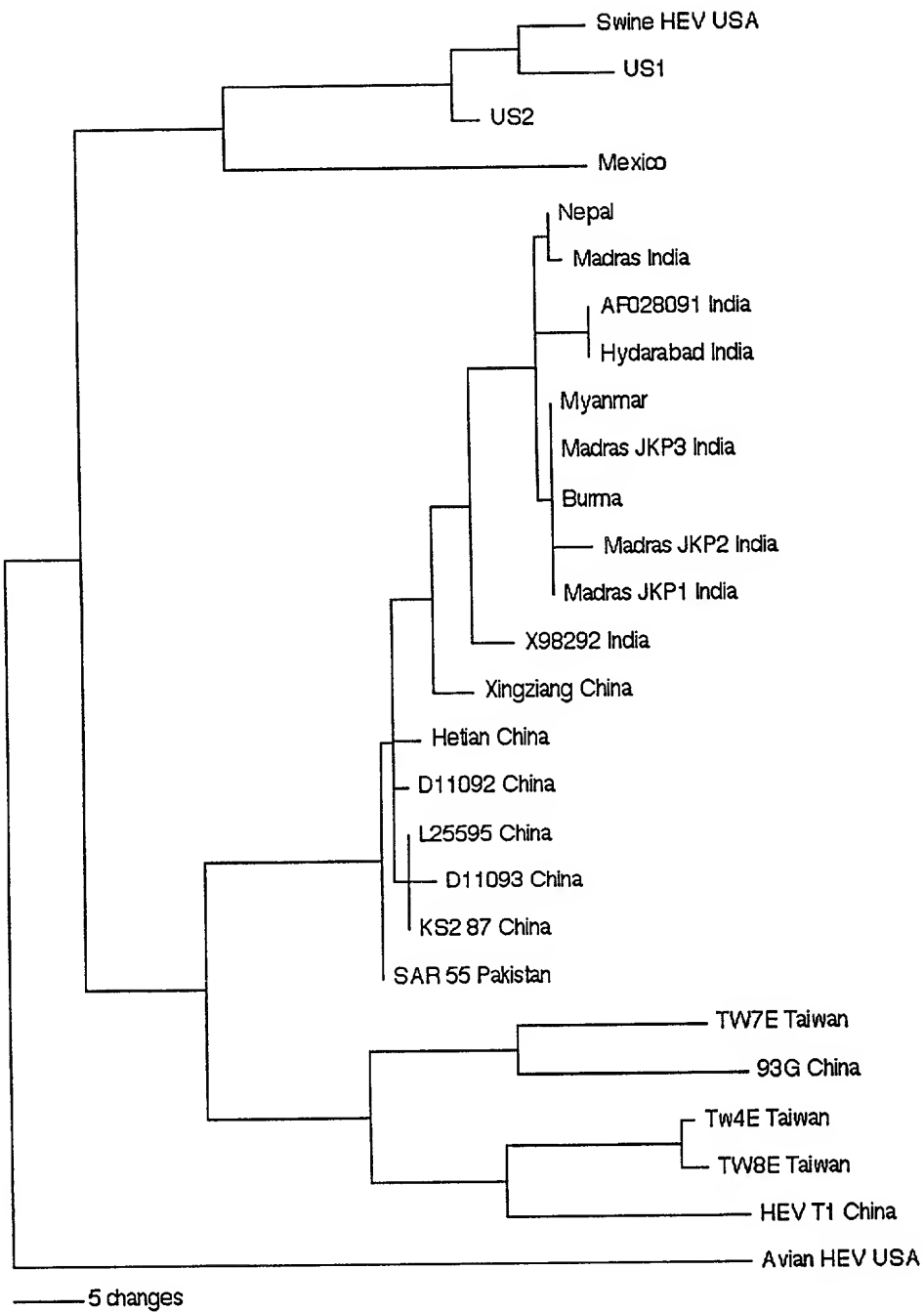


Fig. 8C

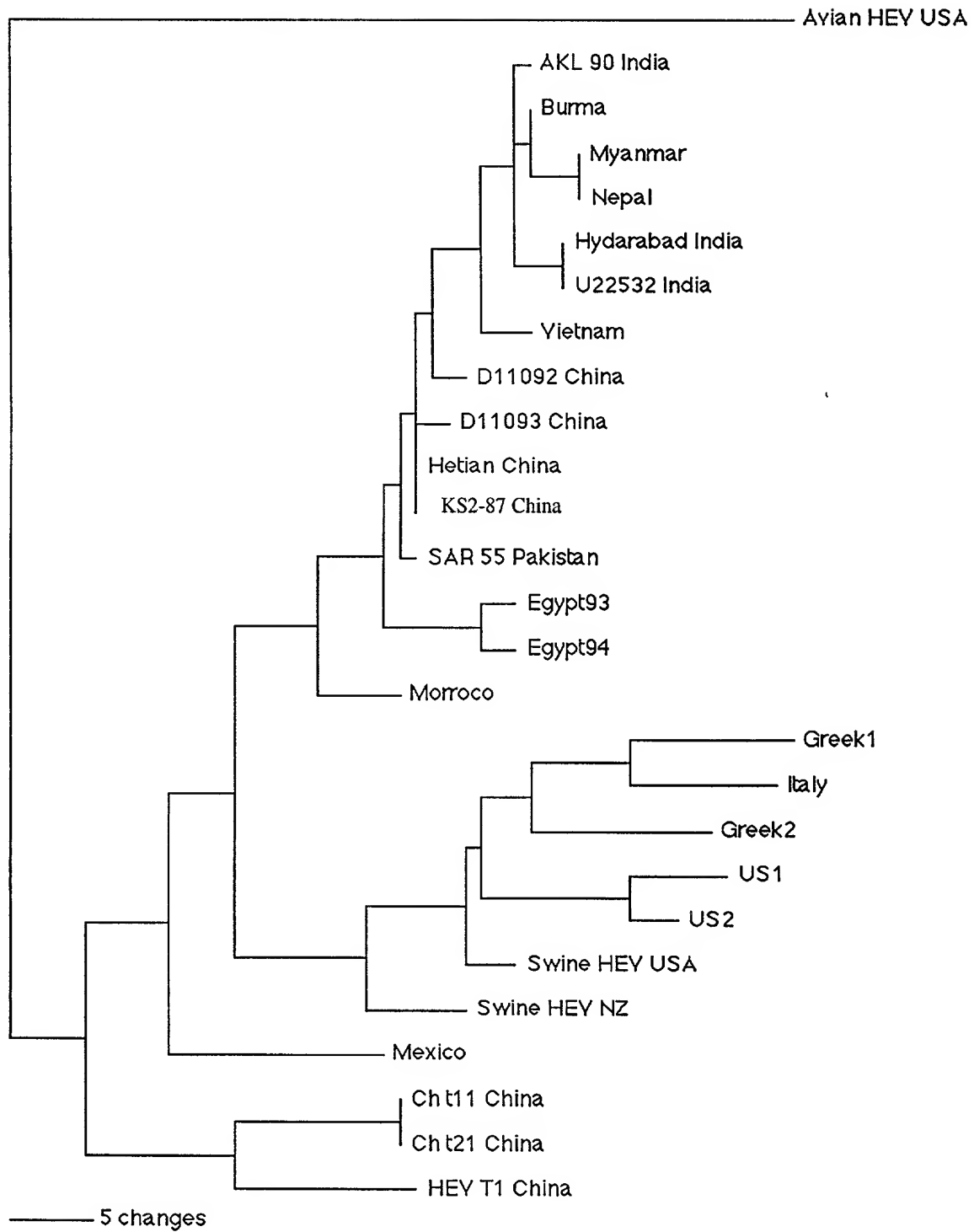


Fig. 9A

ACCAGCATTGGATTTTCGATGGACGCTGTTTAACGAGCGCCGTTGATCTTGGG
TTGCAGCCTACCAGCTGGCGCACCGTATCCCACCGTTGCCCTTGGGACGTTT
GTATATTTTTTGCCTACTGATTATCCGACTATCACCACAACCAGTAGGGTGCT
GCGGTCTGTTGTGTTTACCGGTGAAACCATTGGTCAGAAGATAGTGTTTACC
CAGGTGGCCAAGCAGTCGAACCCCGGGTCCATAACGGTCCATGAGGCGCAG
GGCAGTACTTTTGATCAGACTACTATAATCGCCACGTTAGATGCTCGTGGCC
TTATAGCTTCATCTCGCGCGCATGCCATAGTTGCGCTAACCCGCCACCGGGA
GCGCTGTAGTGTGATTGATGTTGGTGGGGTGCTGGTTCGAGATTGGAGTTACT
GATGCCATGTTTAACAATATCGAAATGCAGCTTGTGCGACCTGATGCTGCAG
CCCCTGCCGGGGTGCTACGAGCCCCAGACGACACCGTGGATGGCTTGTTGGA
CATACCCCGGCCACACTGATGTAGCGGCGGTGTTAACAGCTGAGGCGATT
GGGCATGCGCCCCCTTGAATTGGCCGCCATAAATCCACCCGGGCCTGTATTGG
AGCAGGGCCTATTATACATGCCGGCCAGGCTTGATGGGCGTGATGAGGTTGT
TAAGCTCCAGCTGTCGGATACTGTACACTGCCGCCTGGCTGCACCCACTAGC
CGTCTTGCGGTGATTAACACATTGGTTGGGCGGTACGGTAAAGCCACTAAGC
TGCCTGAGGTTGAATATGACTTAATGGACACTATTGCGCAGTTCTGGCATCA
TATCGGACCAATCAACCCCTCAACACTGGAGTATGCAGAGATGTGCGAGGC
CATGCTTAGTAAGGGCCAGGATGGGTCCCTTGATTGTACATCTGGATTTACAG
GATGCTGATTGTTCTCGCATAACATTCTTCCAGAAGGACTGCGCTAAATTTA
CGCTGGATGACCCTGTTGCACACGGTAAAGTGGGACAGGGGATATCTGCGT
GGCCGAAAACCTTTGTGTGCACTTTTCGGCCCCCTGGTTCCGGGCTATAGAGAA
GCACCTTGTTGGCTGGGTACCCCCAGGTTATTACTATGGGGACCTGTACACG
GAAGCCGATCTGCATCGTTCTGTGCTTTGCGCGCCTGCTGGTCACCTTGTTTT
TGAGAATGATTTCTCAGAGTTTGACTCAACGCAGAATAATGTGTCCCTTGAT
CTCGAATGTGAATTGATGCGCAGGTTTGGGATGCCCCGATTGGATGGTAGCCT
TGTACCATCTTGTTTCGATCATACTGGCTCTTGGTTGCCCCGAAAGAAGCCCTT
CGTGGCTGTTGGAAAAAACACTCTGGTGAGCCGGGCACCCTTTTGTGGAATA
CAGTTTGGAACATGACTGTGTTGCATCATGTTTATGAGTTTGATCGACCAAG
TGTGTTGTGTTTCAAAGGTGATGATAGTGTCTGTGAATCGGTGCGC

Fig. 9B

GCCCGTCCAGAGGGCGTTAGTCTCGTGGCAGACTGCGGGGCTAAAAATGAAG
 GACAAGACCGGCCCGTGTGGCGCCTTTTCCAACCTGCTGATCTTCCCGGGAG
 CTGGTGTGTCTGCGACCTGTTACGGCAGTGGGGCCGCTTGACTGACAAGAA
 CTGGGGGCCCCGACATTCAGCGGATGCAGGACCTTGAGCAAGCGTGTAAGGA
 TTTTGTTCACGTGTTGTAACCTCAGGGTAAAGAGATGTTGACCATCCAGCTT
 GTGGCGGGTTATTATGGTGTGGAAGTTGGTATGGTTGAGGTGGTTTGGGGGG
 CTTTGAAGGCCTGCGCCGCAGCCCGCGAGACCCTAGTGACCAACAGGTTGCC
 GGTACTAAACTTATCTAAGGAGGACTGAACAAATAACAATCATTATGCAGT
 CTGCGCGTCCATGTGCCTTAGCTGCCAGTTCTGGTGTGTTGGAGTGCCAGGAA
 AGTGGGGTGGGATGTCGCTGTGTAGATTGTTGCTCATGCTTGCAATGTGCTG
 CGGGGTGTCAAGGGGCTCCCAAACGCTCCCAGCCGGAGGCAGGCGTGGCCA
 GCGCCGCCGTGACAATTCAGCCCAGTGGAGCACTCAACAACGCCCCGAGGG
 AGCCGTGCGCCCCGCCCCCTCTCACAGACGTTGTCACCGCGGCAGGTACTCGC
 ACGGTACCAGATGTAGATCAAGCCGGTGCCGTGCTGGTGCGCCAGTATAATC
 TAGTGACCAGCCCGTTAGGCCTGGCCACCCTTGGTAGCACCAATGCCTTGCT
 TTATGCCGCACCGGTGTCACCGTTAATGCCGCTTCAGGACGGCACGACGTCT
 AATATCATGAGCACGGAGTCTAGCAACTATGCTCAATACCGTGTACAGGGCC
 TAACTGTCCGCTGGCGCCCAGTTGTGCCAAATGCGGTGGGCGGCTTCTCTAT
 AAGCATGGCCTATTGGCCCCAGACAACATCCACCCCTACAAGCATTGACATG
 AATTCCATCACGTCCACTGACGTCCGTGTGGTGCTTCAGCCGGGCTCTGCTG
 GTTTGCTGACTATACCACATGAGCGTTTGGCGTATAAGAACAATGGTTGGCG
 GTCCGTGCAAACGGTATCCGTCCCACAGGAGGATGCCACGTCCGGCATGCTC
 ATGGTTTGTGTCCACGGGACCCCCTGGAATAGTTATAACCAATAGTGTTTACA
 CCGGGCCGCTTGGTATGGTTGATTTTGCCATAAAGTTACAGCTAAGGAACTT
 GTCGCCCCGTAATACAAATGCCAGGGTCACCCGTGTGAAGGTGACGGCCCC
 ACATACCATCAAGGCTGACCCATCTGGTGCTACCATAACAACAGCAGCTGCG
 GCCAGGTTTATGGCGGATGTGCGTTGGGGCTTGGGCACTGCTGAGGATGGCG
 AAATTGGTCACGGCATCCTTGGTGTCTGTTTAACCTGGCGGACACAGTTTT
 AGGTGGCTTGCCCTCGACACTGCTGCGGGCGGGCGAGTGGTCAGTACATGTAC

Fig. 9C

GGCCGGCCTGTGGGGAACGCGAACGGCGAGCCTGAGGTGAAACTGTATATG
TCGGTTGAGGATGCCGTTAACGATAAACCTATTATGGTCCCCCATGACATCG
ACCTCGGGACCAGCACTGTCACCTGCCAGGACTATGGGAATCAGCATGTGG
ATGACCGCCCATCCCCGGCCCCGGCCCCCTAAGCGAGCTTTGGGCACCCTAAG
GTCAGGGGATGTGTTGCGTATTACTGGCTCCATGCAGTATGTGACTAACGCC
GAGTTGTTACCGCAGAGTGTGTCACAGGGGTACTTTGGGGCCGGCAGCACC
ATGATGGTGCATAATTTGATCACTGGTGTGCGCGCCCCCGCCAGTTCAGTCG
ACTGGACGAAGGCAACAGTGGATGGGGTCCAGGTGAAGACTGTCGATGCTA
GTTCTGGGAGTAATAGGTTTGCAGCGTTACCTGCATTTGGAAAGCCAGCTGT
GTGGGGGGCCCCAGGGCGCTGGGTATTTCTACCAGTATAACAGCACCCACCA
GGAGTGGATTTATTTTCTTCAGAATGGTAGCTCCGTGGTTTGGTATGCATATA
CTAATATGTTGGGCCAGAAGTCAGATACATCCATTCTTTTGGAGGTCCGGCC
AATCCAAGCTAGTGATCAGCCTTGGTTTTTGGCACACCACACTGGCGGCGA
TGACTGTACCACCTGTCTGCCTCTGGGGTTAAGAACATGTTGCCGCCAGGCG
CCAGAAGACCAGTCACCTGAGACGCGCCGGCTCCTAGACCGGCTTAGTAGG
ACATTCCCCTCACCACCCTAATGTCGTGGTTTTTGGGGTTTTAGGTTGATTTTC
TGTATCTGGGCGTAATTGCCCTATGTTTAATTTATTGTGATTTTTATAACTG
TTCATTTGATTATTTATGAAATCCTCCCATCTCGGGCATAGTAAAAAAAAAA
AAAAA

Fig. 10

PALDFDGRCLTSAVDLGLQPTSWRTVSHRCPWDVCIFLRDYP TITTTSRVLRSV
VFTGETIGQKIVFTQVAKQSNPGSITVHEAQGSTFDQTTIIATLDARGLIASSRAH
AIVALTRHRERCSVIDVGGVLVEIGVTDAMFNNIE

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Fig. 11

ACCAGCATTGGATTTTCGATGGACGCTGTTTAACGAGCGCCGTTGATCTTGGG
TTGCAGCCTACCAGCTGGCGCACCGTATCCCACCGTTGCCCTTGGGACGTTT
GTATATTTTTGCGTACTGATTATCCGACTATCACCACAACCAGTAGGGTGCT
GCGGTCTGTTGTGTTTACCGGTGAAACCATTGGTCAGAAGATAGTGTTTACC
CAGGTGGCCAAGCAGTCGAACCCCGGGTCCATAACGGTCCATGAGGCGCAG
GGCAGTACTTTTGATCAGACTACTATAATCGCCACGTTAGATGCTCGTGGCC
TTATAGCTTCATCTCGCGCGCATGCCATAGTTGCGCTAACCCGCCACCGGGA
GCGCTGTAGTGTGATTGATGTTGGTGGGGTGCTGGTTCGAGATTGGAGTTACT
GATGCCATGTTTAACAATATCGAA

Fig. 12

LVRPDAAAPAGVLRAPDDTVDGLLDIPPAHTDVA AVLTAEAIGHAPLELAAINP
PGPVLEQGGLLYMPARLDGRDEVVKLQLSDTVHCRLAAPT SRLAVINTLVGRYG
KATKLPEVEYDLMDTIAQFWHHIGPINPSTLEYAEMCEAMLSKGQDGLIVHLD
LQDADCSRITFFQKDCAKFTLDDPVAHGKVGQGISA WPKTLCALFGPW FRAIEK
HLVAGLPPGYYYGDLYTEADLHRSVLCAPAGHLVFENDFSEFDSTQNNVSLDL
ECEL MRRFGMPDWMVALYHLVRSYWLLVAPKEALRGCWKKHSGEPGTLLWN
TVWNMTVLHHVYEFDRPSVLCFKGDDSVVVCESVRARPEGVSLVAD`CGLKMK
DKTGPCGAFSNLLIFPGAGVVCDLLRQWGRLTDKNWGPDIQRMQDLEQACKDF
VARVVTQGKEMLT IQLVAGYYGVEVGMVEV VWGALKACAAARETLVTNRLP
VLNLSKED

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Fig. 13

gcttgtgcgacctgatgctgcagcccctgccggggtgctacgagccccagacgacaccgtggatggcttgttgacataccc
ccggcccacactgatgtagcggcggtgtaacagctgaggcgattgggcatgcgccccttgaattggccgccataaatccacc
cgggcctgtattggagcagggcctattatacatgccggccaggcttgatgggcgtgatgaggttgtaagctccagctgtcggg
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taaggaggac

Fig. 15

atgtcgtgtgttagattgttgcctcatgcttgaatgtgctgctgggggtgtcaaggggctcccaaacgctcccagccggaggcagg
cgtggccagcgcgcgcgtgacaattcagcccagtgaggcactcaacaacgccccgaggagccgtcggccccgcccctct
cacagacgttgtcaccgcggcaggtactcgcacggtagcatgtagatcaagccggtgccgtgctggtgcgccagtataatc
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acctgagacgcgcggctcctagaccggcttagtaggacattccccaccaccctaa

Fig. 16

MCLSCQFWCLECQESGVGCRCVDCCSCLQCAAGCQGAPKRSQPEAGVASAAV
TIQPSGALNNAPREPSAPPLSQTLSRQVLARYQM

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Fig. 17

atgtgccttagctgccagttctgggtttggagtgccaggaaagtgggggtgggatgtcgcctgtgtagattgttgcctcatgcttgca
atgtgctgcgggggtgtcaaggggctccaaacgctcccagccggaggcaggcgtggccagcgcgcgctgacaattcagc
ccagtggagcactcaacaacgccccgaggggagccgtcggccccgcccctctcacagacgttgtcaccgcggcaggtactcg
cacgggtaccagatgtag

Figure 1. Schematic representation of the structure of the *hsp70* gene. The gene is organized into 11 exons (numbered 1 to 11) and 10 introns (numbered 1 to 10). The exons are represented by boxes, and the introns by lines. The size of each exon and intron is indicated in base pairs (bp) above the boxes and lines, respectively. The positions of the primers used for PCR amplification are indicated by arrows. The primers are numbered 1 to 10, corresponding to the exons they amplify. The positions of the restriction sites for *Xba*I and *Hind*III are indicated by vertical lines. The positions of the *hsp70* gene in the genome are indicated by the numbers 1 to 11.

Fig. 18A



Fig. 18B



40029840-123404

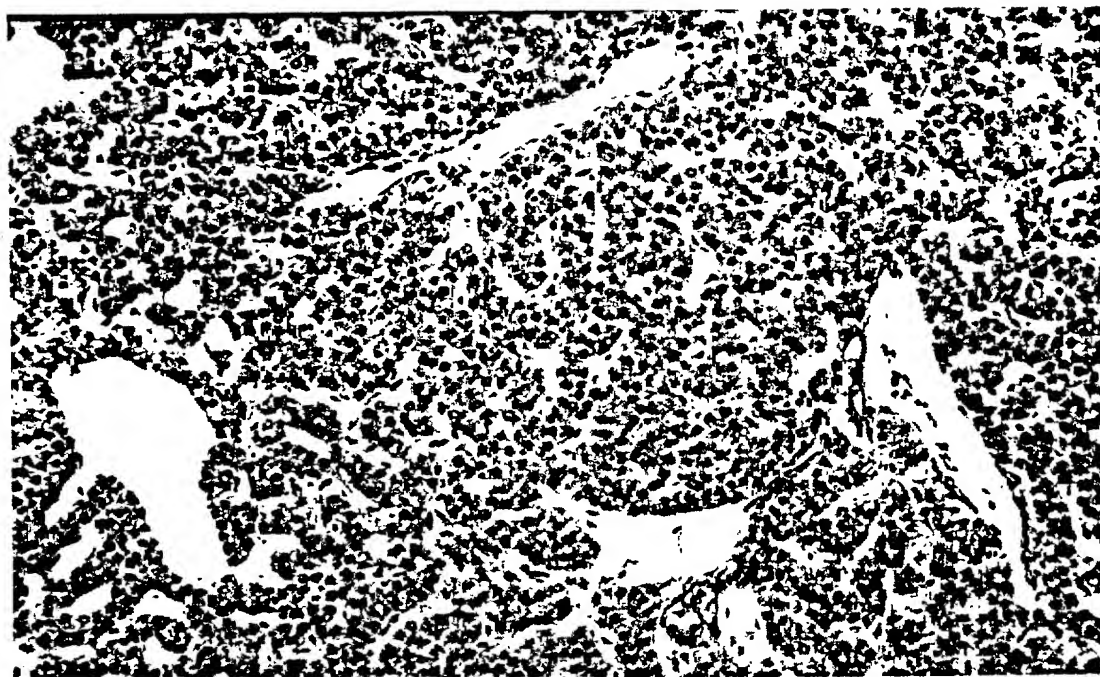


Fig. 19A

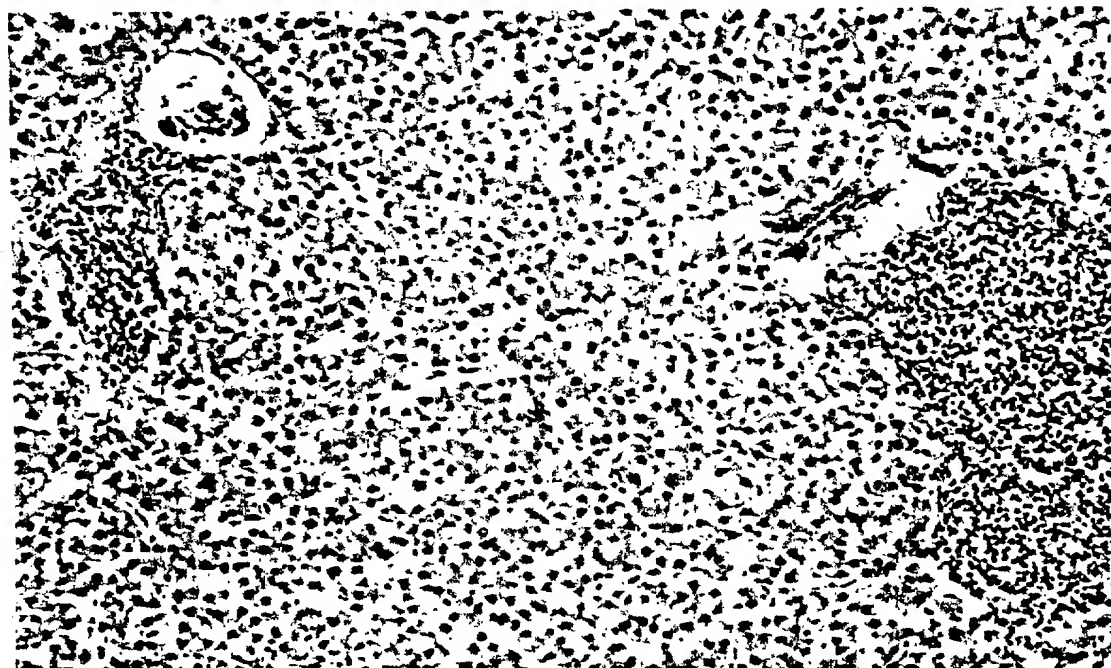


Fig. 19B

Fig. 20

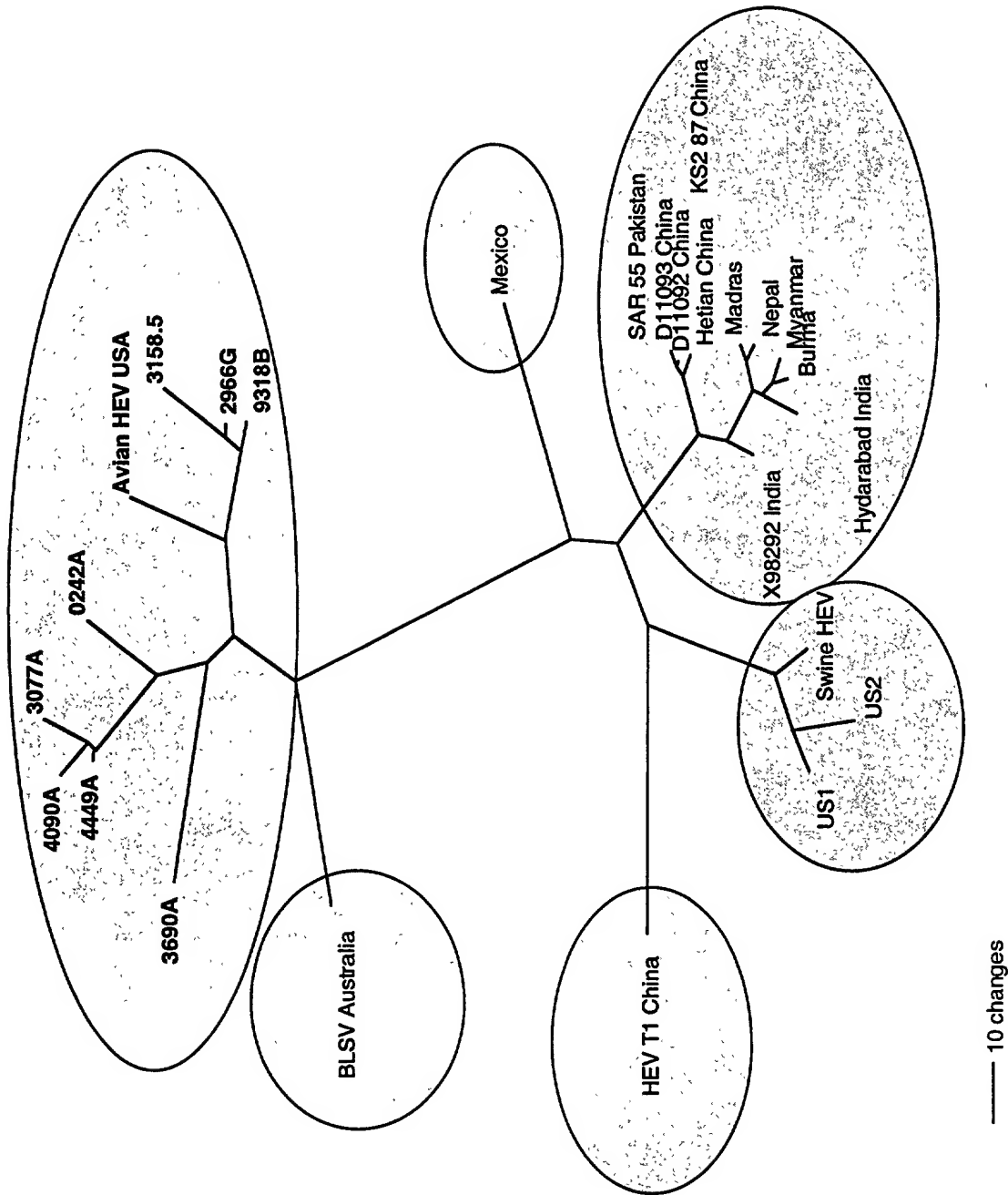
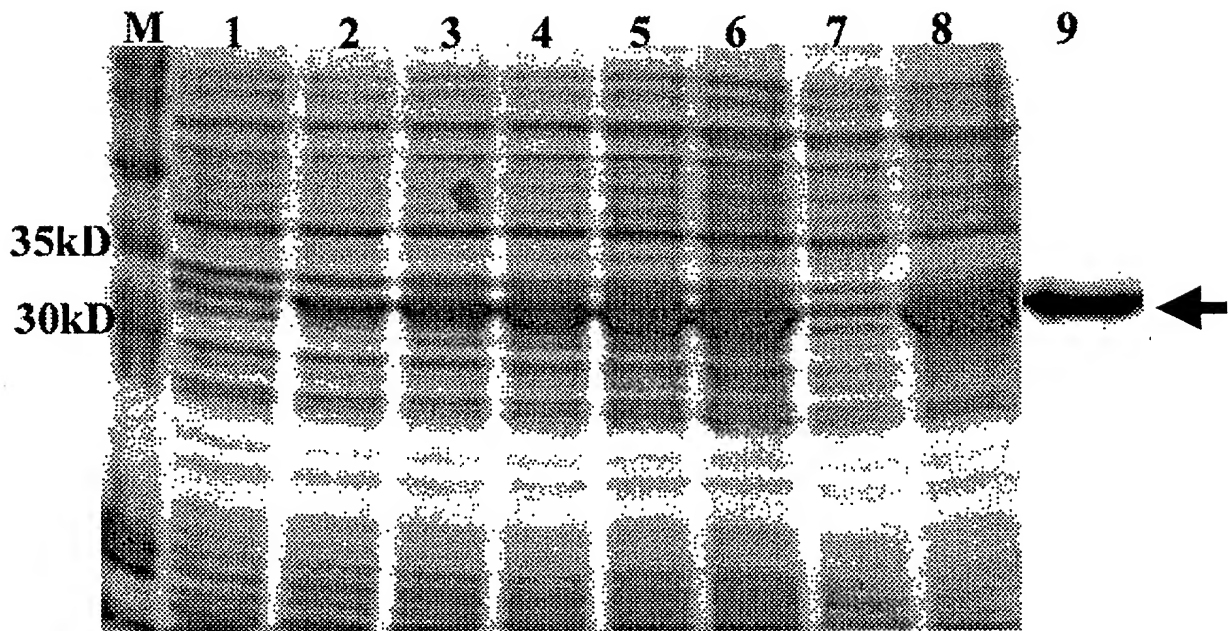


Fig. 21A



1 2 3



Fig. 21B

TOP SECRET - 0486200T

Fig. 22A

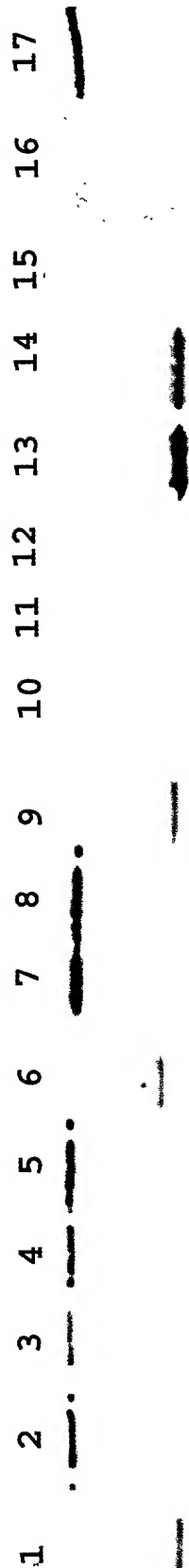


Fig. 22B

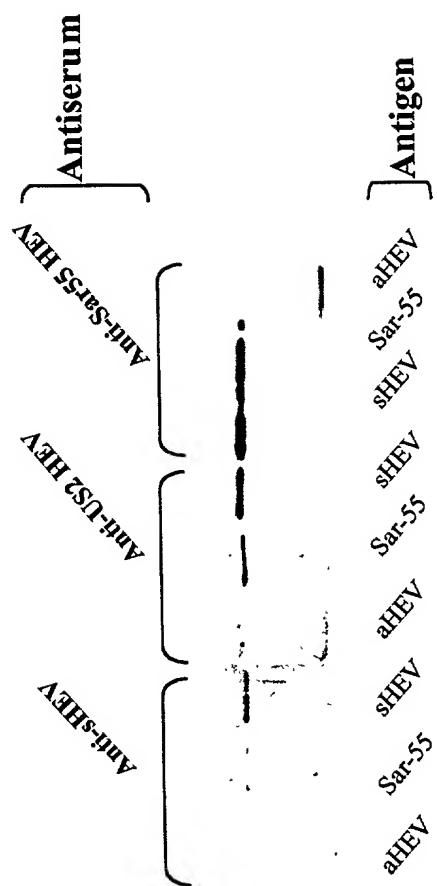


Fig. 22C

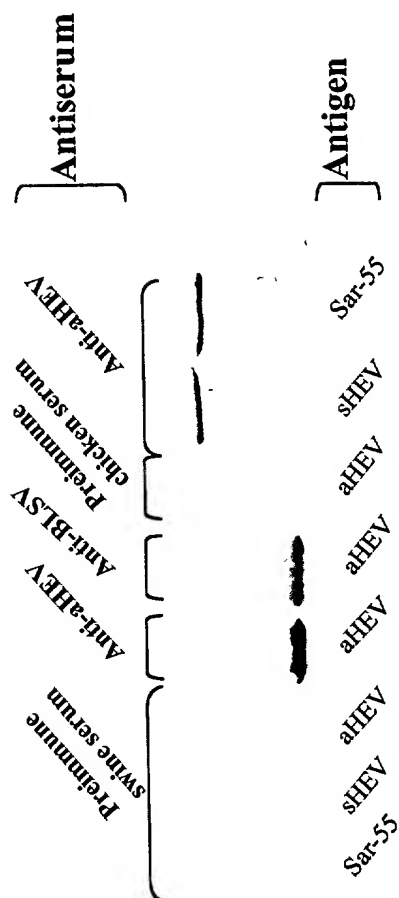


Fig. 23

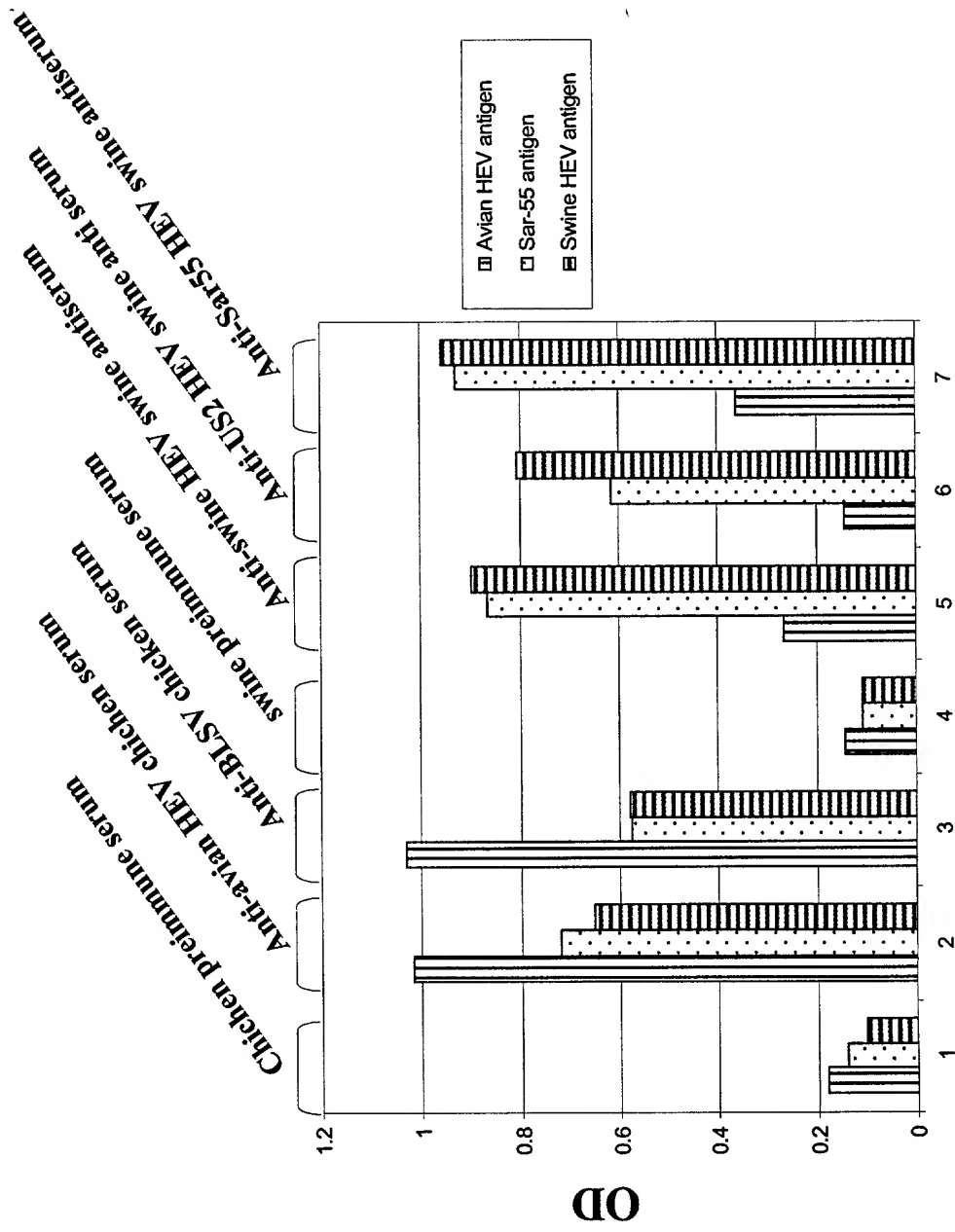


Fig. 24

Avian HEV QYMYGRPVGNANGEPEVKLYMSVEDAVNDKPIMVPHDIDLGTSTVTCQDY
 Swine HEV .LF.S...VS.....T....T...N.QQ..G.TI.....D.R.VI...
 US-2 .LF.S...VS.....T....T...N.QQ..G.TI.....D.R.VI...
 Sar-55 .LF.S...VS.....T....T...N.QQ..G.AI.....E.R.VI...

Avian HEV GNQHVDDRPSPAPAPKRALGTLRSGDVLRLITGSMQYVTNAELLPQSVSQG
 Swine HEV D...EQ...T.S...S.PFSV..AN...WLSLTA---AEYDQTTYGS.TN
 US-2 D...EQ...T.S...S.PFSV..AN...WLSLTA---AEYDQTTYGS.TN
 Sar-55 D...EQ...T.S...S.PFSV..AN...WLSLTA---AEYDQS TYGS.T

Avian HEV YFGAGSTMMVHNLITGVRAPASSVDWTKATVDGVQVKTVDASSGSNRFAAL
 Swine HEV PMYVSD.VTLV.VA..AQ.V.R.L..S.V.L..RPLT.IQQY.KT--.YV.
 US-2 PMYVSD.VTLV.VA..AQ.V.R.L..S.V.L..RPLT.IQQY.KT--.YV.
 Sar-55 PVYVSDSVTLV.VA..AQ.V.R.L....V.L..RPLS.IQQY.KT--.FV.

Avian HEV PAFGKPAVWGP--QGAGYFYQYNSTHQEWIYFLQN-GSSVVWYAYTNMLGQ
 Swine HEV .LR..LSF.EAGTTK...PYN..T.ASDQ.LIENAA.HRVAIST..TS..A
 US-2 .LR..LSF.EAGTTK...PYN..T.ASDQ.LIENAA.HRVAIST..TS..A
 Sar-55 .LR..LSF.EAGTTK...PYN..T.ASDQLLIENAA.HRVAIST..TS..A

Avian HEV K----SDTSILFEVRPIQASDQ--PWFLAHHTGGDDCTTCLPLGLRTCCRQ
 Swine HEV GPTSI.AVG.V.APHSALAVLEDTVDYPARA..FD.F.PE.RT...QG.AF.
 US-2 GPTSI.AVG.V.APHSALAVLEDTIDYPARA..FD.F.PE.RT...QG.AF.
 Sar-55 GPVSI.AVAV.APHSVLALLEDTMDYPARA..FD.F.PE.RP...QG.AF.

Avian HEV APEDQSPETRRLLDRLSRTFPSPP
 Swine HEV S---TIA.LQ..KMKVGK.RE.--
 US-2 S---TIA.LQ..KMKVGK.RE.--
 Sar-55 S---TVA.LQ..KMKVGK.REL--

Fig. 25A

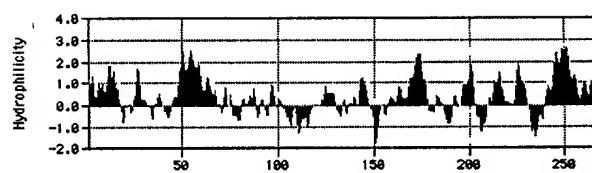
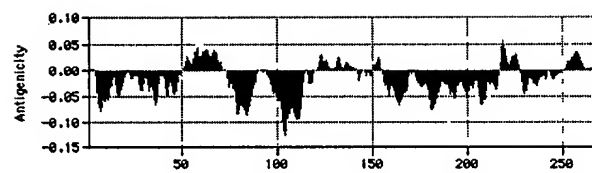


Fig. 25B

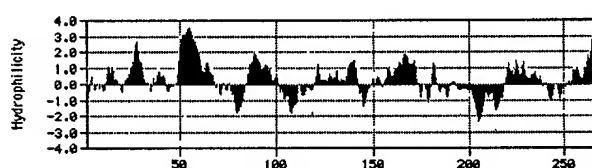
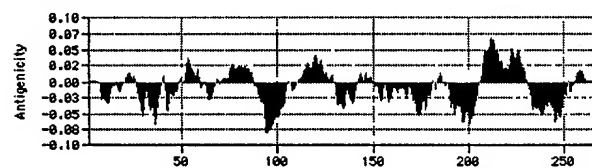


Fig. 25C

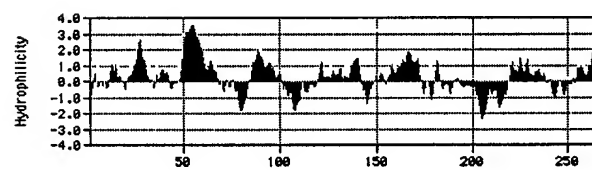
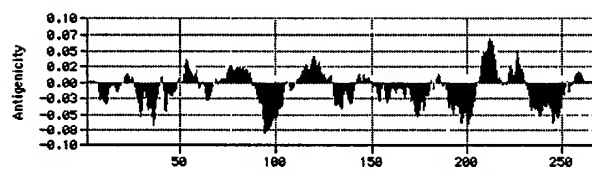


Fig. 25D

